


```

106509
LOCUS      106509               36 bp      DNA      Linear      PAT 02-NOV-1994
DEFINITION Sequence 13 from Patent WO 9002798.
ACCESSION 106509
VERSION   106509.1  GI:589567
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 36)
AUTHORS  Anderson,S., Bennett,W.F., Botstein,D., Higgins,D.L., Paoni,N.F.
          and Zoller,M.
TITLE     TISSUE PLASMINOGEN ACTIVATOR HAVING 77%-GENIC OF FIBRIN SPECIFIC
          PROPERTIES
JOURNAL   Patent: WO 9002798-A 13 22-MAR-1990;
FEATURES  Location/Qualifiers
           source          1..36
           ORGANISM       /organism="unknown"
BASE COUNT 9 a 7 c 8 g 12 t
ORIGIN
Alignment Scores:
Pred. No.: 48.9      Length: 36
Score: 23.00        Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Gaps: 0
DB:
US-09-856-070-25 (1-5) x 106509 (1-36)

QY 1 MetLeuArqLeuGln 5
|||||
DB 15 ATGCTCCGACTGCCA 29

RESULT 2
AX161287
LOCUS      AX161287               51 bp      DNA      Linear      PAT 12-JUN-2001
DEFINITION Sequence 4615 from Patent WO0140521.
ACCESSION AX161287
VERSION   AX161287.1  GI:14542618
KEYWORDS  human.
SOURCE    Human.
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 51)
AUTHORS  Shimkels,R.A. and Leach,M.
TITLE     Nucleic acids containing single nucleotide polymorphisms and
          methods of use thereof
JOURNAL   Patent: WO 0140521-A 4615 07-JUN-2001;
          Curagen Corporation (US)
FEATURES  Location/Qualifiers
           source          1..51
           ORGANISM       /organism="Homo sapiens"
           misc-feature    26
                           db_xref="taxon:9606"
           Note="1 of 2 allelic variants (4614 is other entry)"
           Accession number eg43961283
BASE COUNT 11 a 15 c 14 g 11 t
ORIGIN
Alignment Scores:
Pred. No.: 70.1      Length: 51
Score: 23.00        Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Gaps: 0
DB:
US-09-856-070-25 (1-5) x AX161287 (1-51)

QY 1 MetLeuArqLeuGln 5
|||||
DB 15 ATGCTCCGACTGCCA 29

106509
LOCUS      106509               36 bp      DNA      Linear      PAT 02-NOV-1994
DEFINITION Sequence 13 from Patent WO 9002798.
ACCESSION 106509
VERSION   106509.1  GI:589567
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 36)
AUTHORS  Anderson,S., Bennett,W.F., Botstein,D., Higgins,D.L., Paoni,N.F.
          and Zoller,M.
TITLE     TISSUE PLASMINOGEN ACTIVATOR HAVING 77%-GENIC OF FIBRIN SPECIFIC
          PROPERTIES
JOURNAL   Patent: WO 9002798-A 13 22-MAR-1990;
FEATURES  Location/Qualifiers
           source          1..36
           ORGANISM       /organism="unknown"
BASE COUNT 9 a 7 c 8 g 12 t
ORIGIN
Alignment Scores:
Pred. No.: 48.9      Length: 36
Score: 23.00        Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Gaps: 0
DB:
US-09-856-070-25 (1-5) x 106509 (1-36)

QY 1 MetLeuArqLeuGln 5
|||||
DB 15 ATGCTCCGACTGCCA 29

RESULT 3
AX284883
LOCUS      AX284883               51 bp      DNA      Linear      PAT 20-NOV-2001
DEFINITION Sequence 688 from Patent WO0179556.
ACCESSION AX284883
VERSION   AX284883.1  GI:17045571
KEYWORDS  human.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 51)
AUTHORS  Ellis,J., Brown,J.L., Holt,A. and van Huffel,C.
TITLE     Novel genes, compositions and methods for the identification,
          assessment, prevention, and therapy of human cancers
JOURNAL   Patent: WO 0179556-A 688 25-OCT-2001;
          Millennium Predictive Medicine, Inc. (US)
FEATURES  Location/Qualifiers
           source          1..51
           ORGANISM       /organism="Homo sapiens"
           db_xref="taxon:9606"
BASE COUNT 10 a 15 c 16 g 10 t
ORIGIN
Alignment Scores:
Pred. No.: 70.1      Length: 51
Score: 23.00        Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Gaps: 0
DB:
US-09-856-070-25 (1-5) x AX284883 (1-51)

QY 1 MetLeuArqLeuGln 5
|||||
DB 19 ATGCTCCGACTGCCA 33

RESULT 4
AX135207
LOCUS      AX135207               91 bp      DNA      Linear      PAT 29-MAY-2001
DEFINITION Sequence 15 from Patent WO0132928.
ACCESSION AX135207
VERSION   AX135207.1  GI:14271556
KEYWORDS  human.
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 91)
AUTHORS  Farr,S.
TITLE     Methods of determining individual hypersensitivity to an agent
          Patent: WO 0132928-A 15 19-MAY-2001;
          Phase 1 Molecular Toxicology Inc. (US)
FEATURES  Location/Qualifiers
           source          1..91
           ORGANISM       /organism="Homo sapiens"
           db_xref="taxon:9606"
BASE COUNT 19 a 33 c 11 g 28 t
ORIGIN
Alignment Scores:
Pred. No.: 127      Length: 91
Score: 23.00        Matches: 5
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Gaps: 0
DB:
US-09-856-070-25 (1-5) x AX135207 (1-91)

```

```

QY      1 MetLeuArdLeuGln 5
Db      33 ATGCTCAGGCTTCAA 47

RESULT 5
AX135398/c
LOCUS      AX135398      91 bp      DNA      linear      PAT 29-MAY-2001
DEFINITION Sequence 206 from patent WO0229113
ACCESSION  AX135398
VERSION     AX135398.1 GI:14271747
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 91)
AUTHORS     Farr,S.
TITLE       Methods of determining individual hypersensitivity to an agent
JOURNAL     Patent: WO 012928-A 2001-05-10
JOURNAL     Phase-1 Molecular Toxicology Inc. (US)
FEATURES    Location/Qualifiers
            source          1..91
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
BASE COUNT  28 a 11 c 33 g 19 t
ORIGIN

Alignment Scores:
Pred. No.:      127      Length:      91
Score:          23.00    Matches:      5
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             6          Gaps:         0

US-09-856-070-25 (1-5) x AX135398 (1-91)

QY      1 MetLeuArdLeuGln 5
Db      59 ATGCTCAGGCTTCAA 45

RESULT 6
G44283
LOCUS      G44283      123 bp      DNA      linear      STS 28-JAN-1999
DEFINITION WIAP-3933-STS Human Hudson SANGER Homo sapiens STS genomic,
            sequence tagged site.
ACCESSION  G44283
VERSION     G44283.1 GI:4193209
KEYWORDS    STS.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 123)
AUTHORS     Wang,D.G., Fan,J.B., Siao,C.T., Berne,A., Young,P., Sapolsky,P.,
            Chaudour,G., Perkins,N., Winchester,E., Spencer,J., Kruglyak,L.,
            Stein,L., Hsieh,L., Topaloglou,I., Hubbell,E., Robinson,E.,
            Mittman,M., Morris,M.S., Shen,N., Kilburn,D., Rioux,J.,
            Nusbaum,C., Rozen,S., Hudson,T.I., Lipshutz,P., Chee,M. and
            Lander,E.S.
TITLE       Large-scale identification, mapping, and genotyping of
            single-nucleotide polymorphisms in the human genome
JOURNAL     Science 280 (5360), 1377-1382 (1998)
MEDLINE    98248615
PUBMED     9582121
SYNOPSIS    stS28822
CONTACT     Thomas Hudson
            Whitehead Institute/MIT Center for Genome Research
            Whitehead Institute for Biomedical Research
            9 Cambridge Center, Cambridge MA 02142 USA
            Tel: 617 252 1900
            Fax: 617 252 1902

Email: thudson@genome.wi.mit.edu
Primer A: TGGAGGCTCACTTGAGC
Primer B: ATGCTCAGGCTTCAATTC
STS size: 123
PCR Profile:
    Presoak:          94 degrees C for 4.00 minutes
    Denaturation:     94 degrees C for 50.0 seconds
    Annealing:        58 degrees C for 1.50 minutes
    Polymerization:    72 degrees C for 5.00 minutes
    PCR Cycles:       30
    Thermal Cycler:    custom built by IAS, Costa, Cambridge MA

Protocol:
    Template:         10 ng
    Primers:          each 5 pM
    dNTPs:            4 mM
    Taq Polymerase:    0.5 U
    Total Vol:        20 ul.

Buffer:
    Mg2+:             1.5 mM
    KCl:              50 mM
    Tris-HCl:         10 mM
    Gelatin:          .001 %
    Location/Qualifiers
            source          1..123
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /map="164.70 cM from top of Chr9 linkage group"
            /clone_lib="Human Hudson SANGER"
            /note="human STS created from EST in the Sanger database"
            1..123
            primer_bind     1..18
            primer_bind     40 a 30 c 30 g 22 t 1 others
            BASE COUNT      40 a 30 c 30 g 22 t 1 others
            ORIGIN

Alignment Scores:
Pred. No.:      174      Length:      123
Score:          23.00    Matches:      5
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             11          Gaps:         0

US 09 856-070-25 (1-5) x G44283 (1-123)

QY      1 MetLeuArdLeuGln 5
Db      24 ATGCTCAGGCTTCAA 38

RESULT 7
AX135708
LOCUS      AX135708      129 bp      DNA      linear      PAT 29-JUN 2002
DEFINITION Sequence 4123 from Patent WO0229113.
ACCESSION  AX135708
VERSION     AX135708.1 GI:21660516
KEYWORDS
SOURCE      Bacillus licheniformis.
            Bacillus licheniformis
            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE   1
AUTHORS     Berka,R. and Clausen,I.G.
TITLE       Methods for monitoring multiple gene expression
JOURNAL     Patent: WO 0229113-A 4123 11-Apr 2002;
            Novozymes Biotech, Inc. (US) ; Novozymes A/S (DK)
FEATURES    Location/Qualifiers
            source          1..129
            /organism="Bacillus licheniformis"
            /db_xref="taxon:1402"
BASE COUNT  27 a 40 c 29 g 33 t
ORIGIN

Alignment Scores:

```

```

Pred. No.: 184 Length: 129
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-070-25 (1-5) x AX135709 (1-129)

QY 1 MetLeuArqLeuGln 5
Db 66 AGTTACGACTTCAA 80

RESULT 8
LOCUS 065968 150 bp DNA linear STS 02-NOV-2001
DEFINITION s806 Miscellaneous Y sequences Homo sapiens STS genomic sequence
tagged site.
ACCESSION 065968
VERSION 065968.1 GI:15078019
KEYWORDS STS
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 150)
AUTHORS Tilford, G.A., Kuroda-Kawaguchi, T., Skolnik, H., Pozen, S.,
Brown, L.G., Rosenberq, M., McPherson, I.D., Wylie, K., Sekhon, M.,
Kucaba, T.A., Waterston, R.H., and Page, D.C.
TITLE A physical map of the human Y chromosome
JOURNAL Nature 409 (6822), 943-945 (2001)
MEDLINE 21131744
PUBMED 11237016
COMMENT Contact: Tomoko Kawauchi
Page Lab
Whitehead Institute for Biomedical Research
Room 423, 9 Cambridge Center, Cambridge, MA 02142, USA
Email: kawauchi@wi.mit.edu
Primer A: TGTAAGTGAAGGAGAGGATGG
Primer B: AGGAACAAAGGAGGACATTGC
STS size: 150
PCR Profile:
94C 3:00 min
55x / 94C 1:00 sec
1:00 min
72C 1:00 min
5:00 min

Protocol: Template: 1 ul saturated bacterial culture (HACs) or 100
ng DNA

Primer: each 1 uM
dNTPs: each 100 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 15 ul or 20 ul
Mineral Oil: 15 ul

Buffer: For 20ml of 10x Stock solution.
Stock Reagent Volume Mixed Final Conc. of 10x Stock
1M KCl 10 ml 500 mM
1M Tris-HCl, pH 9.0 2 ml 100 mM
Triton X-100 200 ul 1.0 %
2M MgCl2 150 ul 15 mM
H2O 7.65 ml.
Location/Qualifiers
1. 150
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone.lib="Miscellaneous Y sequences"
/proc="human STS derived from miscellaneous Y sequences"
1. 150
primer_bind 1. 120

```

```

primer_bind 38 a 26 c 43 g 43 t
BASE COUNT complement(130..150)
ORIGIN
Alignment Scores:
Pred. No.: 213 Length: 150
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-856-070-25 (1-5) x 065968 (1-150)

QY 1 MetLeuArqLeuGln 5
Db 04 ATTGTGAATTATAG 80

RESULT 9
LOCUS AX135383 173 bp DNA linear PAT 29-MAY-2001
DEFINITION Sequence 191 from Patent WO9132928.
ACCESSION AX135383
VERSION AX135383.1 GI:14271712
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 173)
AUTHORS Farr, S.
TITLE Methods of determining individual hypersensitivity to an agent
JOURNAL Patent: WO 0132928-A 191 10-MAY-2001;
Phase-1 Molecular Toxicology Inc. (US)
FEATURES Location/Qualifiers
source 1..173
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 59 a 25 c 40 g 49 t
ORIGIN
Alignment Scores:
Pred. No.: 247 Length: 173
Score: 23.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-070-25 (1-5) x AX135383 (1-173)

QY 1 MetLeuArqLeuGln 5
Db 67 AGCTGGCGCTTCAA 81

RESULT 10
LOCUS ASA012135/c 176 bp DNA linear PIN 05-JAN-2001
DEFINITION Avena sativa mitochondrial cp-like trna-ser (GSA) gene.
ACCESSION AJ012135
VERSION AJ012135.1 GI:12057053
KEYWORDS transfer RNA-Ser; trna-ser gene.
SOURCE cat.
ORGANISM Mitochondrion Avena sativa
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae;
Pooidae; Avenae; Avena.
REFERENCE 1 (bases 1 to 176)
AUTHORS Rainaldi, G.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 176)
AUTHORS Rainaldi, G.
TITLE Direct Submission

```

JOURNAL: Submitted (14-OCT-1998) Rainaldi G., Dipartimento di Biochimica e Biologia Molecolare, Universita' di Bari, via Grubona 4, 70125 BARI, ITALY

FEATURES
 source
 1. .176
 /organism="Homo sapiens"
 /orquellio="Mitochondrion"
 /db_xref="taxon:4498"
 57. .143
 /gene="LNA-Ser (GGA)"
 57. .143
 /gene="tRNA-Ser (GGA)"
 /product="tRNA-Ser"
 /evidence experimental

BASE COUNT 48 a 32 c 42 g 54 t

ORIGIN

Alignment Scores:
 Pred. No.: 252 Length: 176
 Score: 23.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 9
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-09-856-070-25 (1-5) x ASA012135 (1-176)

QY 1 MetLeuArgLeuGln 5
 |||||

Db 89 ATGCTAGCGCTTCAA 75

RESULT 11

HAJ9282 180 bp DNA linear PRI 04-NOV-1998
 LOCUS HAJ9282/2
 DEFINITION Homo sapiens translocation t(11;22) DNA in twings's tumor derivative 11 (isolate: EWTUM23/cha).

ACCESSION AJ229282
 VERSION AJ229282.1 GI:3849897
 KEYWORDS EWS; FLI-1; translocation.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 180)
 AUTHORS Zucman-Rossi, J., Lejoux, F., Virelizier, J. M., Leclerc, B. and Thomas, J.
 TITLE Chromosome translocation based on illegitimate recombination in human tumors
 JOURNAL: Proc. Natl. Acad. Sci. U.S.A. 95 (20), 11786-11791 (1998)
 MEDLINE 98426231
 PUBMED 9751743
 REFERENCE 2 (bases 1 to 180)
 AUTHORS Zucman-Rossi, J.
 TITLE Direct Submission
 JOURNAL: Submitted (27 MAY 1998) Zucman-Rossi J., INSERM U434/CEPH, 27 rue Juliette Lodu, 75010 Paris, FRANCE

FEATURES
 source
 1. .180
 /organism="Homo sapiens"
 /isolate="EWTUM23/cha"
 /db_xref="taxon:9606"
 /tissue.type="Cervix's tumor"
 /note="derivative 11"
 1. .103
 /gene="FLI-1"
 <1. .103
 /gene="FLI-1"
 /note="Y17293: location 44761-44863"
 106. .180
 /gene="EWS"
 106. .>180
 /gene="EWS"
 /note="Y08806: location 39688-39762"

BASE COUNT 55 a 22 c 44 g 59 t

ORIGIN

Alignment Scores:
 Pred. No.: 257 Length: 180
 Score: 23.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-856-070-25 (1-5) x HAJ9282 (1-180)

QY 1 MetLeuArgLeuGln 5
 |||||

Db 74 ATGTTAGATTACAG 60

RESULT 12

GI2522 632522 185 bp LNA linear SIS 24-SEP-1999
 DEFINITION A309066 Human HOMO sapiens STS genomic, sequence tagged site.
 ACCESSION GI2522
 VERSION GI2522.1 GI:5923043
 KEYWORDS STS.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 186)
 AUTHORS Adams, M.D.
 TITLE Human STS sequences
 JOURNAL: Unpublished (1996)
 COMMENT Contact: Mark Adams
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Email: mdadams@tigr.org
 Primer A: AGTACGGTTACAGGTATATGTC
 Primer B: AGTGGATCATGCCCTGTA
 STS size: 186
 PCR Profile:
 Denaturation: 96C 5min
 Anneal: 54C 30sec
 Extend: 72C 30sec
 Denature: 95C 30sec
 FinalExtend: 72C 5min
 Cycles: 30
 Protocol:
 GenomicDNA: 25 ng
 Primer: 0.43 uM each
 dNTPs: 230 uM each
 AmpliTaq: 0.5 units
 TaqStart Ab: 0.5 units
 Total Volume: 10 uL
 Buffer:
 Tris-HCl pH8.8: 100 mM
 KCl: 500 mM
 MgCl2: 20 mM
 Triton X-100: 1%
 Concentration: 10X
 Prepared with primer pairs derived from HGI12360, GenBank
 Accession Numbers: P57885, R2414, L65722.
 FEATURES
 source
 1. .186
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Human"
 1. .186
 primer_bind 1. .23
 primer_bind complement(169..186)
 BASE COUNT 35 a 48 c 37 g 66 t
 ORIGIN

```

Alignment Scores:
  Pred. No.: 266 Length: 186
  Score: 24.00 Matches: 5
  Percent Similarity: 100.00% Conservative: 0
  Best Local Similarity: 100.00% Mismatches: 0
  Query Match: 100.00% Indels: 0
  Gaps: 0
  DB: 11

US-09-856-070-25 (1-5) x G32522 (1-186)

QY 1 MetLeuArqLeuGln 5
DB 159 ATGCTGACACTGCAA 174

RESULT 14
AF103945
LOCUS Sus scrofa CCAAT/enhancer binding protein beta 209 bp mRNA linear MAM 09-MAR-1999
DEFINITION Sus scrofa CCAAT/enhancer binding protein beta (C/EBP beta) mRNA.
ACCESSION AF103945
VERSION 1
KEYWORDS Sus scrofa
SOURCE Sus scrofa
ORGANISM Sus scrofa
REFERENCE 1 (bases 1 to 209)
AUTHORS Ding, S.T. and Mersmann, H.J.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-1998) Pediatrics, Baylor College of Medicine,
1100 Bates St., Houston, TX 77030, USA
FEATURES
    Location/Qualifiers
        1..209
            /organism="Sus scrofa"
            /db_xref="taxon:9823"
            /c1..209
            /gene="C/EBP beta"
            /c1..209
            /gene="C/EBP beta"
            /codon_start=2
            /product="CCAAT/enhancer binding protein beta"
            /protein_id="AA019576.1"
            /db_xref="GI:4378475"
            /translation="KKIVIKKHSQFYKIKKKNNIAVKKSKAKAKMNLKIQKVLKLI
            AENERLOKKVEQISRELSLRLNLFK"
BASE COUNT 59 a 59 c 69 q 22 t
ORIGIN
Alignment Scores:
  Pred. No.: 300 Length: 209
  Score: 24.00 Matches: 5
  Percent Similarity: 100.00% Conservative: 0
  Best Local Similarity: 100.00% Mismatches: 0
  Query Match: 100.00% Indels: 0
  Gaps: 0
  DB: 4

US-09-856-070-25 (1-5) x AF103945 (1-209)

QY 1 MetLeuArqLeuGln 5
DB 115 ATGCTGACACTGCAA 101

RESULT 15
G26672/c
LOCUS human STS STS_M63154, sequence tagged site.
DEFINITION human STS STS_M63154, sequence tagged site.
ACCESSION G26672
VERSION G26672.1 GI:1348904
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens STSs derived from sequences in dbEST and the Unique
collection.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 212)
AUTHORS Hudson, I.
TITLE Whitehead Institute/MIT Center for Genome Research: Physically
Mapped STSs
JOURNAL unpublished (1995)
COMMENT
    Contact: Thomas Hudson
    Whitehead Institute/MIT Center for Genome Research
    Whitehead Institute for Biomedical Research
    9 Cambridge Center, Cambridge MA 02142 USA
    tel: 617 252 1900
    Fax: 617 252 1902
    Email: thudson@genome.wi.mit.edu
    Primer A: TGGGTTCAAGCTTCTATCAAAACA
    Primer B: ATGAGTCATAGATGTGACACTCCA
    STS size: 178

```

PCR Profile:
 Pre-soak:
 Denaturation:
 Annealing: 56 degrees C
 Polymerization:
 PCR Cycles: 35
 Thermal Cycler:
 Protocol:
 Template: 10 ng
 Primer: each 5 pM
 dNTPs: each 4 mM
 Taq Polymerase: 0.025 units/ul
 Total Vol: 20 ul
 Buffer:
 MgCl2: 1.5 mM
 KCl: 50 mM
 Tris-HCl: 10 mM
 pH: 9.3

FEATURES
 source
 1. .212
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="317.2 cR from top of Chr11 linkage group"
 STS
 primer_bind 12. .189
 primer_bind 12. .33
 primer_bind complement(165. .189)
 BASE COUNT 75 a 40 c 35 g 62 t
 ORIGIN

Alignment Scores:
 Pred. No.: 305 Length: 212
 Score: 23.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-09-856-070-25 (1-5) x 926672 (1 212)

OY 1 MetLeuArgLeuGln 5
 Db 178 ATGTGAGACTGAG 164

Search completed: January 16, 2003, 19:05:57
 Job time : 443.214 secs

